

21437  
Ser. No.  
09/529,043

SEQUENCE LISTING

<110> Forschungszentrum Juelich GmbH

<120> Method for microbial production of amino acids of the aspartate and/or glutamate family and agents which can be used in said method

<130> 1

<140> 09/529,043

<141> 2000-04-03

<150> PCT/EP98/06210

<151> 1998-09-30

<160> 4

<170> PatentIn Ver. 2.1

<210> 1

<211> 3728

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (165)..(3587)

<223> pyruvate carboxylase

<400> 1  
cgcaaccgtg cttgaagtcg tgcaggtcag gggagtggtg cccgaaaaca ttgagaggaa 60

aacaaaaacc gatgtttgat tgggggaatc ggggggttac atactaggac gcagtgactg 120

ctatcacct tggcgggtctc ttgttgaaag gaataattac tcta gtg tcg act cac 176  
Val Ser Thr His  
1

aca tct tca acg ctt cca gca ttc aaa aag atc ttg gta gca aac cgc 224  
Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu Val Ala Asn Arg  
5 10 15 20

ggc gaa atc gcg gtc cgt gct ttc cgt gca gca ctc gaa acc ggt gca 272  
Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu Glu Thr Gly Ala  
25 30 35

gcc acg gta gct att tac ccc cgt gaa gat cgg gga tca ttc cac cgc 320



Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly Ser Phe His Arg  
 40 45 50

tct ttt gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc 368  
 Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val  
 55 60 65

aag gcg tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt 416  
 Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val  
 70 75 80

aaa gca gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc 464  
 Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala  
 85 90 95 100

cag ctt gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca 512  
 Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro  
 105 110 115

acc cca gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc 560  
 Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr  
 120 125 130

gcc gcg aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc 608  
 Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser  
 135 140 145

aaa aac atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc 656  
 Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro  
 150 155 160

atc ttt gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt 704  
 Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly Arg Gly Met Arg Phe  
 165 170 175 180

gtt gct tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt 752  
 Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg  
 185 190 195

gaa gct gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct 800  
 Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala  
 200 205 210

gtg att aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act 848  
 Val Ile Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr  
 215 220 225

gga gaa gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt 896

Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg  
 230 235 240

cac caa aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa 944  
 His Gln Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu  
 245 250 255 260

ctg cgt gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att 992  
 Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile  
 265 270 275

ggt tac cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc 1040  
 Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly  
 280 285 290

aac cac gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc 1088  
 Asn His Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr  
 295 300 305

gtg act gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc 1136  
 Val Thr Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg  
 310 315 320

ttg gct gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag 1184  
 Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys  
 325 330 335 340

atc aag acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat 1232  
 Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp  
 345 350 355

cca aac aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc 1280  
 Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg  
 360 365 370

tca cca ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt 1328  
 Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly  
 375 380 385

ggc gaa atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc 1376  
 Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys  
 390 395 400

cgt ggt tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg 1424  
 Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu  
 405 410 415 420

gct gag ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt 1472

Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg	
425	430 435
gcg ttg ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga	1520
Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly	
440	445 450
ttc att gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat	1568
Phe Ile Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp	
455	460 465
gag cag gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag	1616
Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys	
470	475 480
cct cat ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg	1664
Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu	
485	490 495 500
cct aac atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc ctg	1712
Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg Leu	
505	510 515
aag cag ctt ggc cca gcc gcg ttt gct cgt gat ctc cgt gag cag gac	1760
Lys Gln Leu Gly Pro Ala Ala Phe Ala Arg Asp Leu Arg Glu Gln Asp	
520	525 530
gca ctg gca gtt act gat acc acc ttc cgc gat gca cac cag tct ttg	1808
Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala His Gln Ser Leu	
535	540 545
ctt gcg acc cga gtc cgc tca ttc gca ctg aag cct gcg gca gag gcc	1856
Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro Ala Ala Glu Ala	
550	555 560
gtc gca aag ctg act cct gag ctt ttg tcc gtg gag gcc tgg ggc ggc	1904
Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu Ala Trp Gly Gly	
565	570 575 580
gcg acc tac gat gtg gcg atg cgt ttc ctc ttt gag gat ccg tgg gac	1952
Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp	
585	590 595
agg ctc gac gag ctg cgc gag gcg atg ccg aat gta aac att cag atg	2000
Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln Met	
600	605 610
ctg ctt cgc ggc cgc aac acc gtg gga tac acc ccg tac cca gac tcc	2048

Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp Ser	
615	620 625
gtc tgc cgc gcg ttt gtt aag gaa gct gcc agc tcc ggc gtg gac atc	2096
Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile	
630	635 640
ttc cgc atc ttc gac gcg ctt aac gac gtc tcc cag atg cgt cca gca	2144
Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala	
645	650 655 660
atc gac gca gtc ctg gag acc aac acc gcg gta gcc gag gtg gct atg	2192
Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala Met	
665	670 675
gct tat tct ggt gat ctc tct gat cca aat gaa aag ctc tac acc ctg	2240
Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu	
680	685 690
gat tac tac cta aag atg gca gag gag atc gtc aag tct ggc gct cac	2288
Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His	
695	700 705
atc ttg gcc att aag gat atg gct ggt ctg ctt cgc cca gct gcg gta	2336
Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val	
710	715 720
acc aag ctg gtc acc gca ctg cgc cgt gaa ttc gat ctg cca gtg cac	2384
Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val His	
725	730 735 740
gtg cac acc cac gac act gcg ggt ggc cag ctg gca acc tac ttt gct	2432
Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe Ala	
745	750 755
gca gct caa gct ggt gca gat gct gtt gac ggt gct tcc gca cca ctg	2480
Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala Ser Ala Pro Leu	
760	765 770
tct ggc acc acc tcc cag cca tcc ctg tct gcc att gtt gct gca ttc	2528
Ser Gly Thr Thr Ser Gln Pro Ser Leu Ser Ala Ile Val Ala Ala Phe	
775	780 785
gcg cac acc cgt cgc gat acc ggt ttg agc ctc gag gct gtt tct gac	2576
Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp	
790	795 800
ctc gag ccg tac tgg gaa gca gtg cgc gga ctg tac ctg cca ttt gag	2624

Leu Glu Pro Tyr Trp	Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu	
805	810	815 820
tct gga acc cca ggc cca acc ggt cgc gtc tac cgc cac gaa atc cca		2672
Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro		
825	830	835
ggc gga cag ttg tcc aac ctg cgt gca cag gcc acc gca ctg ggc ctt		2720
Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr Ala Leu Gly Leu		
840	845	850
gcg gat cgt ttc gaa ctc atc gaa gac aac tac gca gcc gtt aat gag		2768
Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala Ala Val Asn Glu		
855	860	865
atg ctg gga cgc cca acc aag gtc acc cca tcc tcc aag gtt gtt ggc		2816
Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly		
870	875	880
gac ctc gca ctc cac ctc gtt ggt gcg ggt gtg gat cca gca gac ttt		2864
Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe		
885	890	895 900
gct gcc gat cca caa aag tac gac atc cca gac tct gtc atc gcg ttc		2912
Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe		
905	910	915
ctg cgc ggc gag ctt ggt aac cct cca ggt ggc tgg cca gag cca ctg		2960
Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu		
920	925	930
cgc acc cgc gca ctg gaa ggc cgc tcc gaa ggc aag gca cct ctg acg		3008
Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr		
935	940	945
gaa gtt cct gag gaa gag cag gcg cac ctc gac gct gat gat tcc aag		3056
Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys		
950	955	960
gaa cgt cgc aat agc ctc aac cgc ctg ctg ttc ccg aag cca acc gaa		3104
Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu		
965	970	975 980
gag ttc ctc gag cac cgt cgc cgc ttc ggc aac acc tct gcg ctg gat		3152
Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp		
985	990	995
gat cgt gaa ttc ttc tac ggc ctg gtc gaa ggc cgc gag act ttg atc		3200

Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile  
 1000 1005 1010

cgc ctg cca gat gtg cgc acc cca ctg ctt gtt cgc ctg gat gcg atc 3248  
 Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile  
 1015 1020 1025

tct gag cca gac gat aag ggt atg cgc aat gtt gtg gcc aac gtc aac 3296  
 Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn  
 1030 1035 1040

ggc cag atc cgc cca atg cgt gtg cgt gac cgc tcc gtt gag tct gtc 3344  
 Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val  
 1045 1050 1055 1060

acc gca acc gca gaa aag gca gat tcc tcc aac aag ggc cat gtt gct 3392  
 Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala  
 1065 1070 1075

gca cca ttc gct ggt gtt gtc acc gtg act gtt gct gaa ggt gat gag 3440  
 Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu  
 1080 1085 1090

gtc aag gct gga gat gca gtc gca atc atc gag gct atg aag atg gaa 3488  
 Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu  
 1095 1100 1105

gca aca atc act gct tct gtt gac ggc aaa atc gat cgc gtt gtg gtt 3536  
 Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp Arg Val Val Val  
 1110 1115 1120

cct gct gca acg aag gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc 3584  
 Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser  
 1125 1130 1135 1140

taa acctttctgt aaaaagcccc gcgtcttcct catggaggag gcggggccttt 3637

ttgggccaaag atgggagatg ggtgagttgg atttggtctg attcgacact tttaagggca 3697

gagatttgaa gatggagacc aaggctcaaa g 3728

<210> 2

<211> 1140

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

Val	Ser	Thr	His	Thr	Ser	Ser	Thr	Leu	Pro	Ala	Phe	Lys	Lys	Ile	Leu
1				5				10						15	
Val	Ala	Asn	Arg	Gly	Glu	Ile	Ala	Val	Arg	Ala	Phe	Arg	Ala	Ala	Leu
		20						25					30		
Glu	Thr	Gly	Ala	Ala	Thr	Val	Ala	Ile	Tyr	Pro	Arg	Glu	Asp	Arg	Gly
	35						40					45			
Ser	Phe	His	Arg	Ser	Phe	Ala	Ser	Glu	Ala	Val	Arg	Ile	Gly	Thr	Glu
	50				55						60				
Gly	Ser	Pro	Val	Lys	Ala	Tyr	Leu	Asp	Ile	Asp	Glu	Ile	Ile	Gly	Ala
65				70					75					80	
Ala	Lys	Lys	Val	Lys	Ala	Asp	Ala	Ile	Tyr	Pro	Gly	Tyr	Gly	Phe	Leu
			85					90						95	
Ser	Glu	Asn	Ala	Gln	Leu	Ala	Arg	Glu	Cys	Ala	Glu	Asn	Gly	Ile	Thr
		100						105					110		
Phe	Ile	Gly	Pro	Thr	Pro	Glu	Val	Leu	Asp	Leu	Thr	Gly	Asp	Lys	Ser
	115					120						125			
Arg	Ala	Val	Thr	Ala	Ala	Lys	Lys	Ala	Gly	Leu	Pro	Val	Leu	Ala	Glu
	130					135					140				
Ser	Thr	Pro	Ser	Lys	Asn	Ile	Asp	Glu	Ile	Val	Lys	Ser	Ala	Glu	Gly
145				150					155					160	
Gln	Thr	Tyr	Pro	Ile	Phe	Val	Lys	Ala	Val	Ala	Gly	Gly	Gly	Gly	Arg
			165					170						175	
Gly	Met	Arg	Phe	Val	Ala	Ser	Pro	Asp	Glu	Leu	Arg	Lys	Leu	Ala	Thr
		180						185					190		
Glu	Ala	Ser	Arg	Glu	Ala	Glu	Ala	Ala	Phe	Gly	Asp	Gly	Ala	Val	Tyr
	195					200						205			
Val	Glu	Arg	Ala	Val	Ile	Asn	Pro	Gln	His	Ile	Glu	Val	Gln	Ile	Leu
	210				215						220				
Gly	Asp	His	Thr	Gly	Glu	Val	Val	His	Leu	Tyr	Glu	Arg	Asp	Cys	Ser
225				230					235					240	
Leu	Gln	Arg	Arg	His	Gln	Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His
			245						250					255	
Leu	Asp	Pro	Glu	Leu	Arg	Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys	Phe
		260						265					270		
Cys	Arg	Ser	Ile	Gly	Tyr	Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu	Val
	275					280						285			
Asp	Glu	Lys	Gly	Asn	His	Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile	Gln
	290				295						300				
Val	Glu	His	Thr	Val	Thr	Glu	Glu	Val	Thr	Glu	Val	Asp	Leu	Val	Lys
305				310					315					320	
Ala	Gln	Met	Arg	Leu	Ala	Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly	Leu
			325						330					335	
Thr	Gln	Asp	Lys	Ile	Lys	Thr	His	Gly	Ala	Ala	Leu	Gln	Cys	Arg	Ile
		340						345					350		
Thr	Thr	Glu	Asp	Pro	Asn	Asn	Gly	Phe	Arg	Pro	Asp	Thr	Gly	Thr	Ile
	355					360						365			
Thr	Ala	Tyr	Arg	Ser	Pro	Gly	Gly	Ala	Gly	Val	Arg	Leu	Asp	Gly	Ala



370	375	380
Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu Val		
385	390	395
Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg Ala		
	405	410
Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn Ile		
	420	425
Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg		
	435	440
Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala Pro		
	450	455
Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val		
465	470	475
Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala Pro		
	485	490
Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser		
	500	505
Arg Asp Arg Leu Lys Gln Leu Gly Pro Ala Ala Phe Ala Arg Asp Leu		
	515	520
Arg Glu Gln Asp Ala Leu Ala Val Thr Asp Thr Thr Phe Arg Asp Ala		
	530	535
His Gln Ser Leu Leu Ala Thr Arg Val Arg Ser Phe Ala Leu Lys Pro		
545	550	555
Ala Ala Glu Ala Val Ala Lys Leu Thr Pro Glu Leu Leu Ser Val Glu		
	565	570
Ala Trp Gly Gly Ala Thr Tyr Asp Val Ala Met Arg Phe Leu Phe Glu		
	580	585
Asp Pro Trp Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val		
	595	600
Asn Ile Gln Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro		
	610	615
Tyr Pro Asp Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser		
625	630	635
Gly Val Asp Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln		
	645	650
Met Arg Pro Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala		
	660	665
Glu Val Ala Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys		
	675	680
Leu Tyr Thr Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys		
	690	695
Ser Gly Ala His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg		
705	710	715
Pro Ala Ala Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp		
	725	730
Leu Pro Val His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala		
	740	745
Thr Tyr Phe Ala Ala Ala Gln Ala Gly Ala Asp Ala Val Asp Gly Ala		

755	760	765
Ser Ala Pro Leu Ser Gly Thr	Thr Ser Gln Pro Ser Leu Ser Ala Ile	
770	775	780
Val Ala Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu		
785	790	795
Ala Val Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr		
805	810	815
Leu Pro Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg		
820	825	830
His Glu Ile Pro Gly Gly Gln Leu Ser Asn Leu Arg Ala Gln Ala Thr		
835	840	845
Ala Leu Gly Leu Ala Asp Arg Phe Glu Leu Ile Glu Asp Asn Tyr Ala		
850	855	860
Ala Val Asn Glu Met Leu Gly Arg Pro Thr Lys Val Thr Pro Ser Ser		
865	870	875
Lys Val Val Gly Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp		
885	890	895
Pro Ala Asp Phe Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser		
900	905	910
Val Ile Ala Phe Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp		
915	920	925
Pro Glu Pro Leu Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys		
930	935	940
Ala Pro Leu Thr Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala		
945	950	955
Asp Asp Ser Lys Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro		
965	970	975
Lys Pro Thr Glu Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr		
980	985	990
Ser Ala Leu Asp Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg		
995	1000	1005
Glu Thr Leu Ile Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg		
1010	1015	1020
Leu Asp Ala Ile Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val		
1025	1030	1035
Ala Asn Val Asn Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser		
1045	1050	1055
Val Glu Ser Val Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys		
1060	1065	1070
Gly His Val Ala Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala		
1075	1080	1085
Glu Gly Asp Glu Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala		
1090	1095	1100
Met Lys Met Glu Ala Thr Ile Thr Ala Ser Val Asp Gly Lys Ile Asp		
1105	1110	1115
Arg Val Val Val Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile		
1125	1130	1135
Val Val Val Ser		

1140

<210> 3  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 3  
cgtcttcac gaaatgaac

19

<210> 4  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: PCR primer

<400> 4  
acggtggtga tccggcact

19